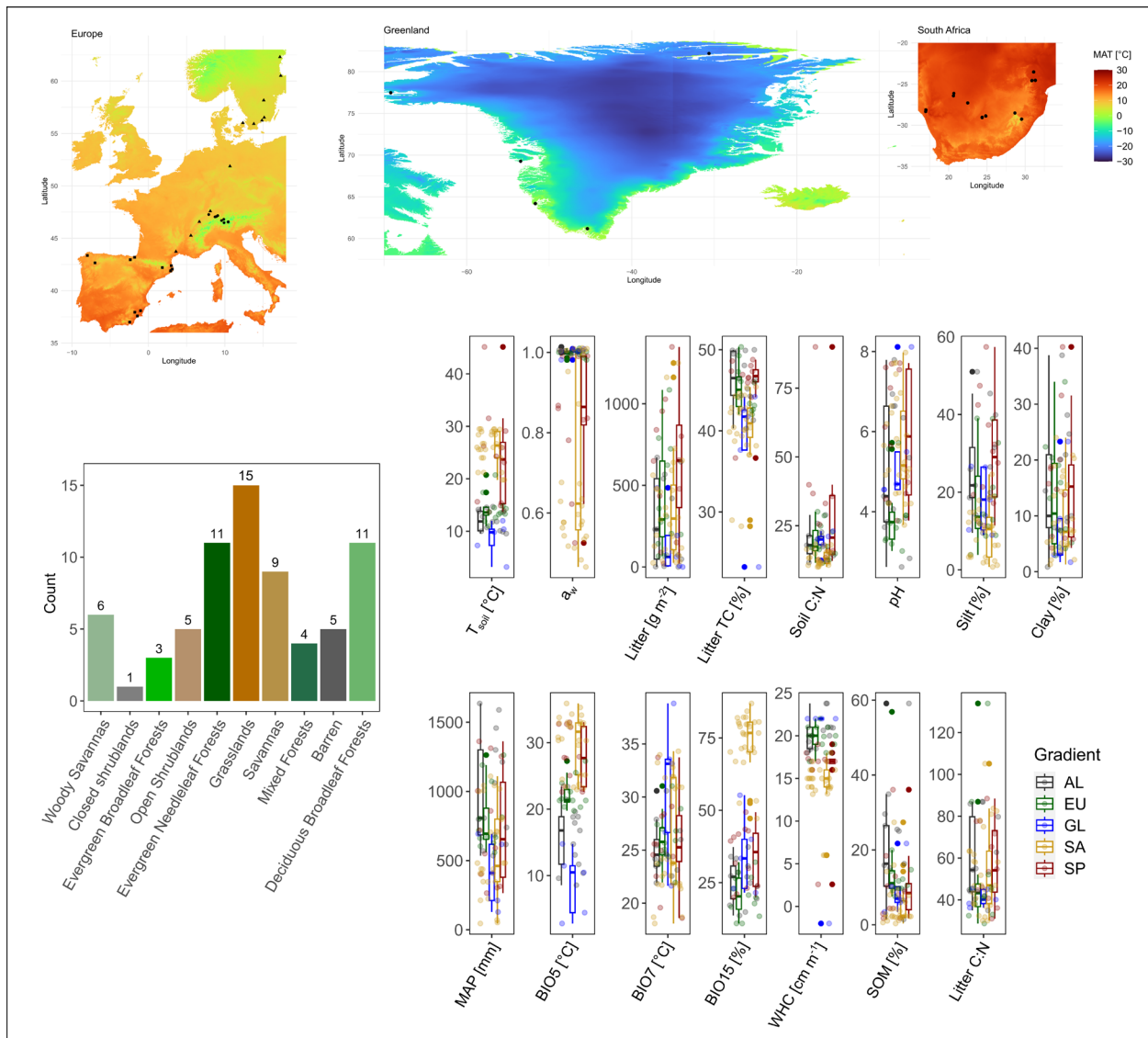
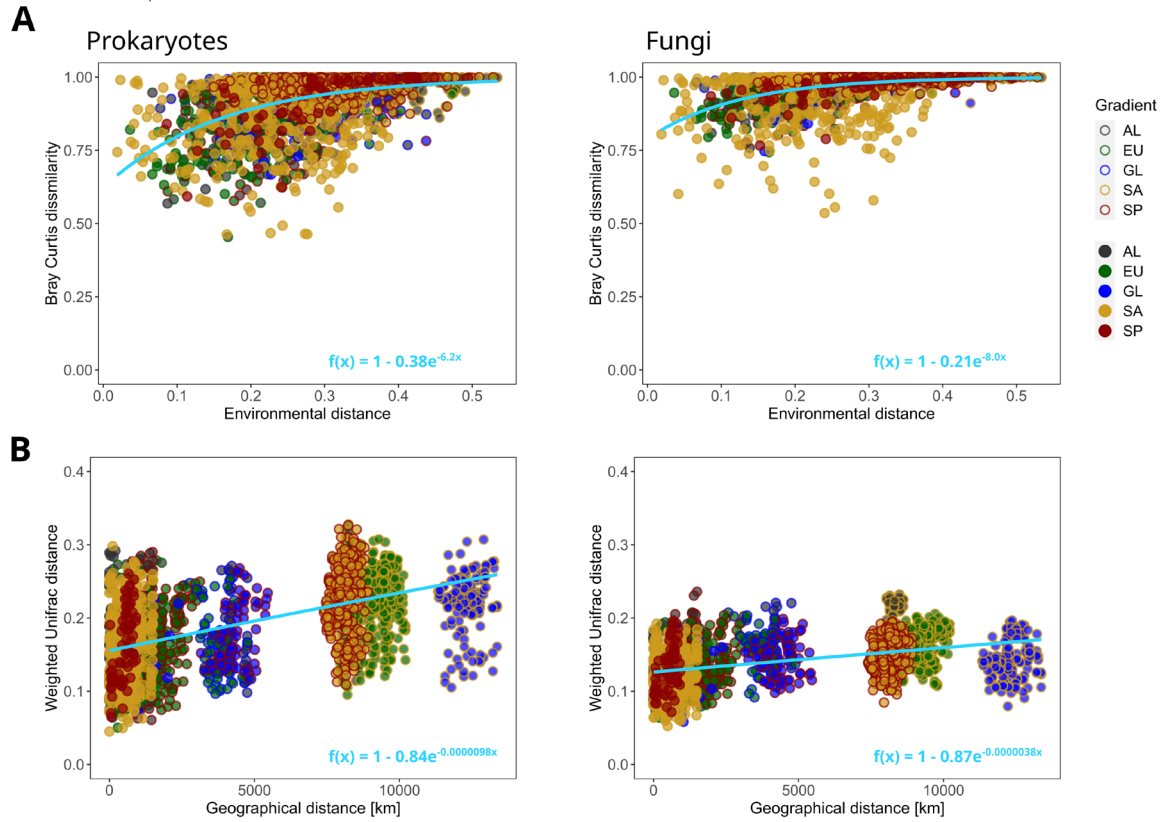


# Supplementary figures and tables

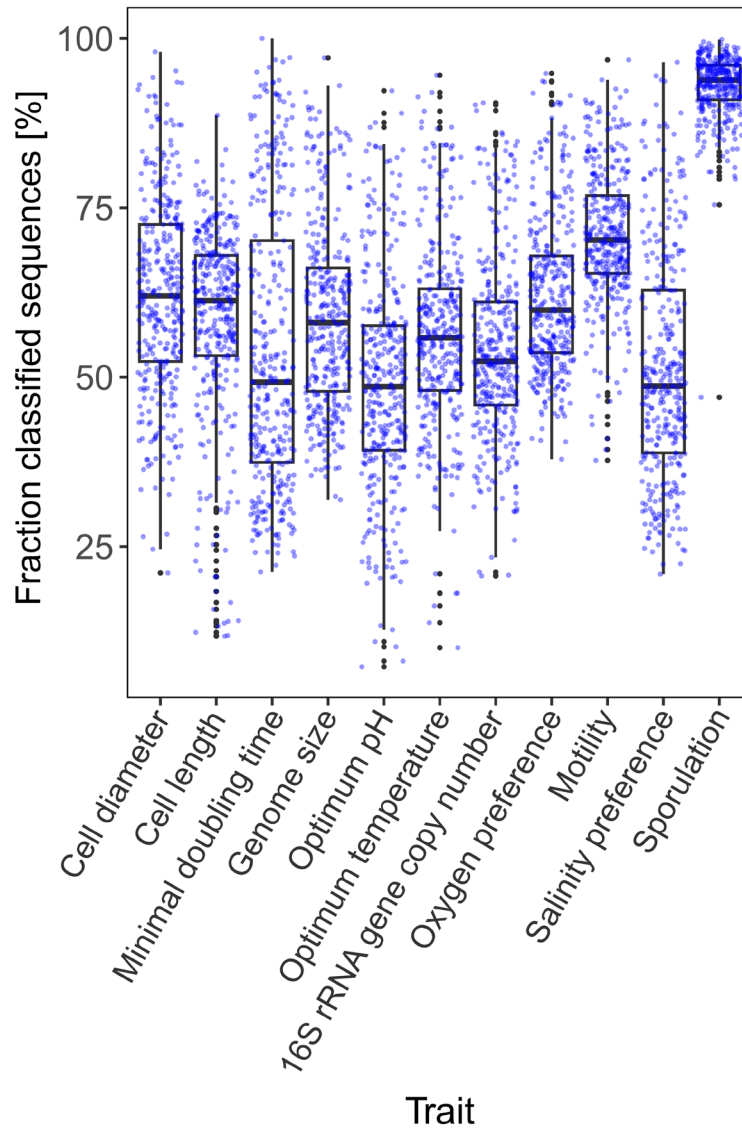
## Figures



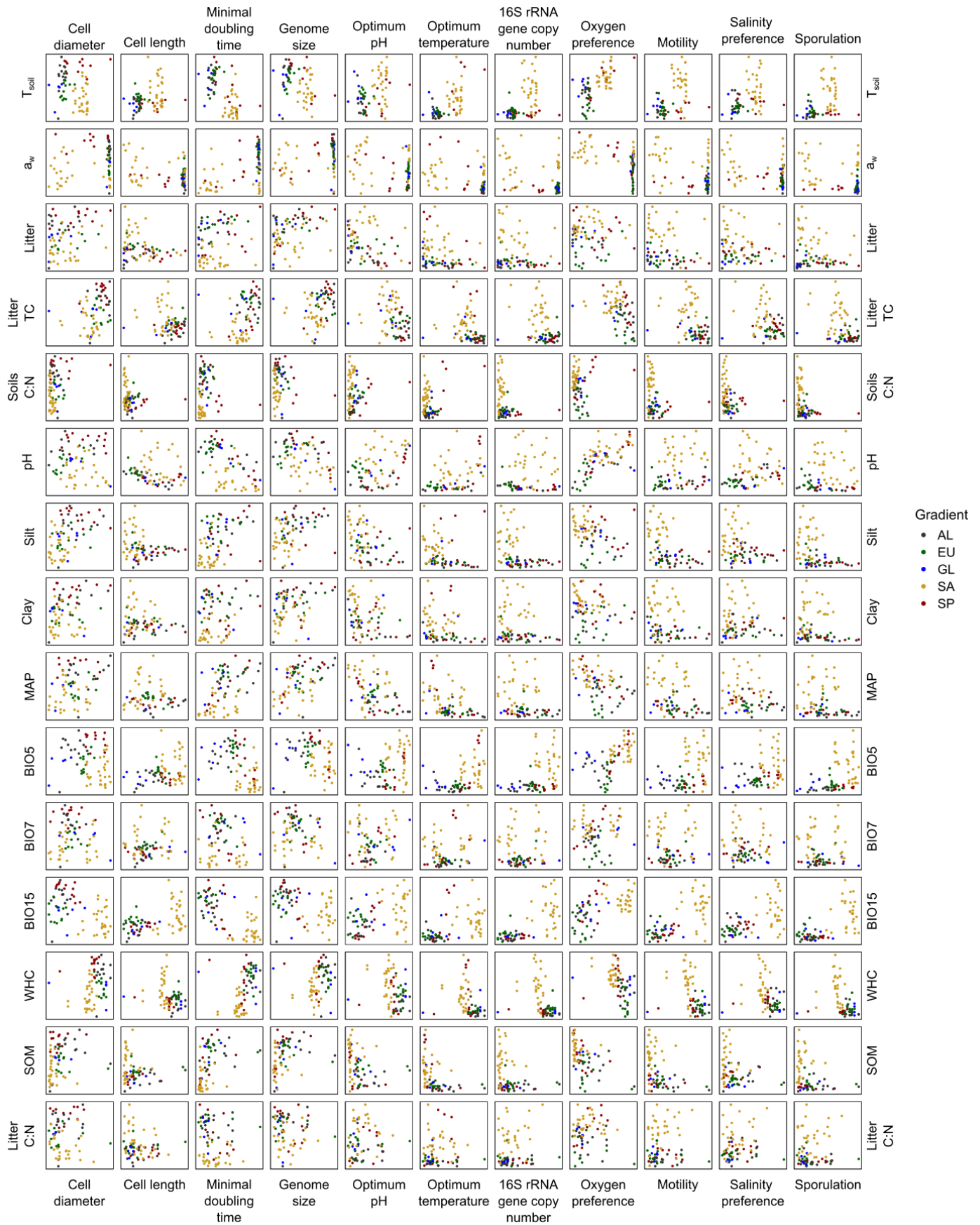
**Figure S1** Climatic, vegetation and soil properties of the sites. Numbers on top of bars indicate sites per land cover class. The central mark of the boxplots indicates the median, upper and lower limits of boxes indicate the 25th and the 75th percentile. AL = alpine, EU = Europe, GL = Greenland, SA = South Africa, SP = Spain,  $a_w$  = water activity, BIO5 = maximum temperature warmest month, BIO15 = precipitation seasonality, LC = land cover, MAP = mean annual precipitation, MAT = mean annual temperature, SOM = soil organic matter, TC = total carbon, TOC = total organic carbon,  $T_{soil}$  = in situ soil temperature at the time of sampling, WHC = water holding capacity.



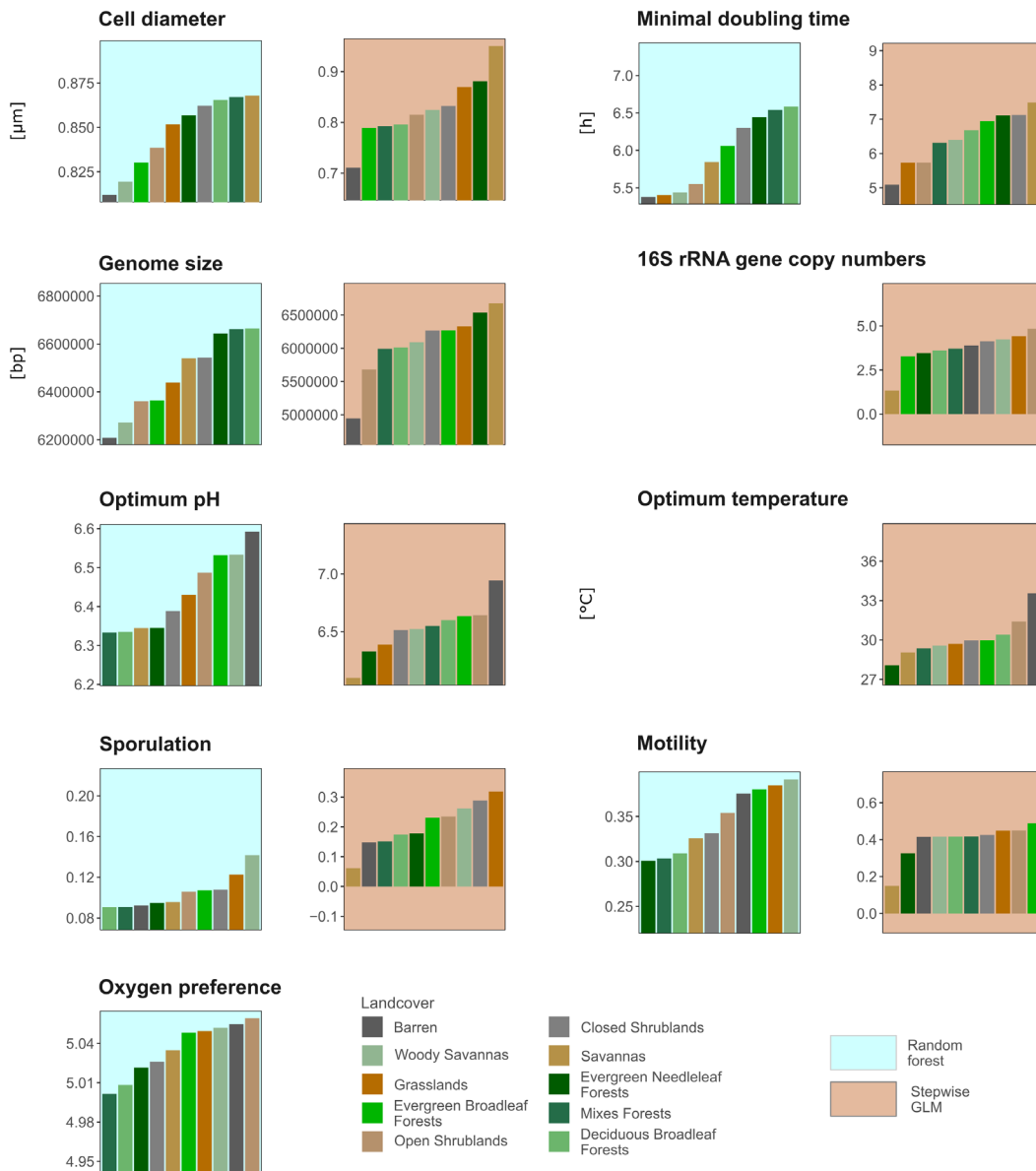
**Figure S2** Distance decay for prokaryotic (left) and fungal community structures (right) based on environmental distances (**A**) and weighted UniFrac distances (**B**). Environmental distances represent Gower distances based on non-colinear environmental variables. Curves were fitted with an exponential model,  $f(x)$  denotes the fitted decay function  $1 - ae^{-bx}$ . Fill and edge color indicate the gradients from which samples were compared.



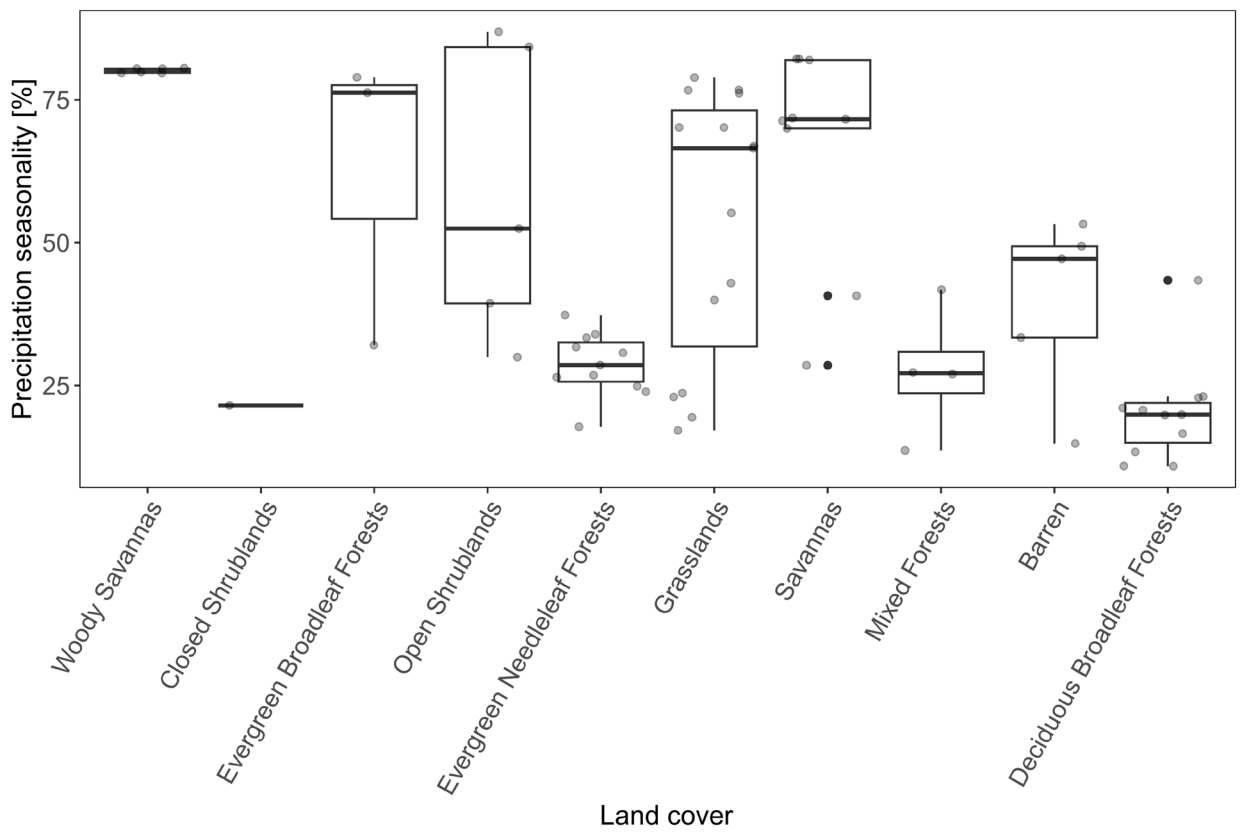
**Figure S3** Fraction of classified sequences for each trait. The central mark indicates the median, upper and lower limits of boxes indicate the 25th and the 75th percentile. Blue points represent samples, 70 sites with 5 replicates (n = 349).



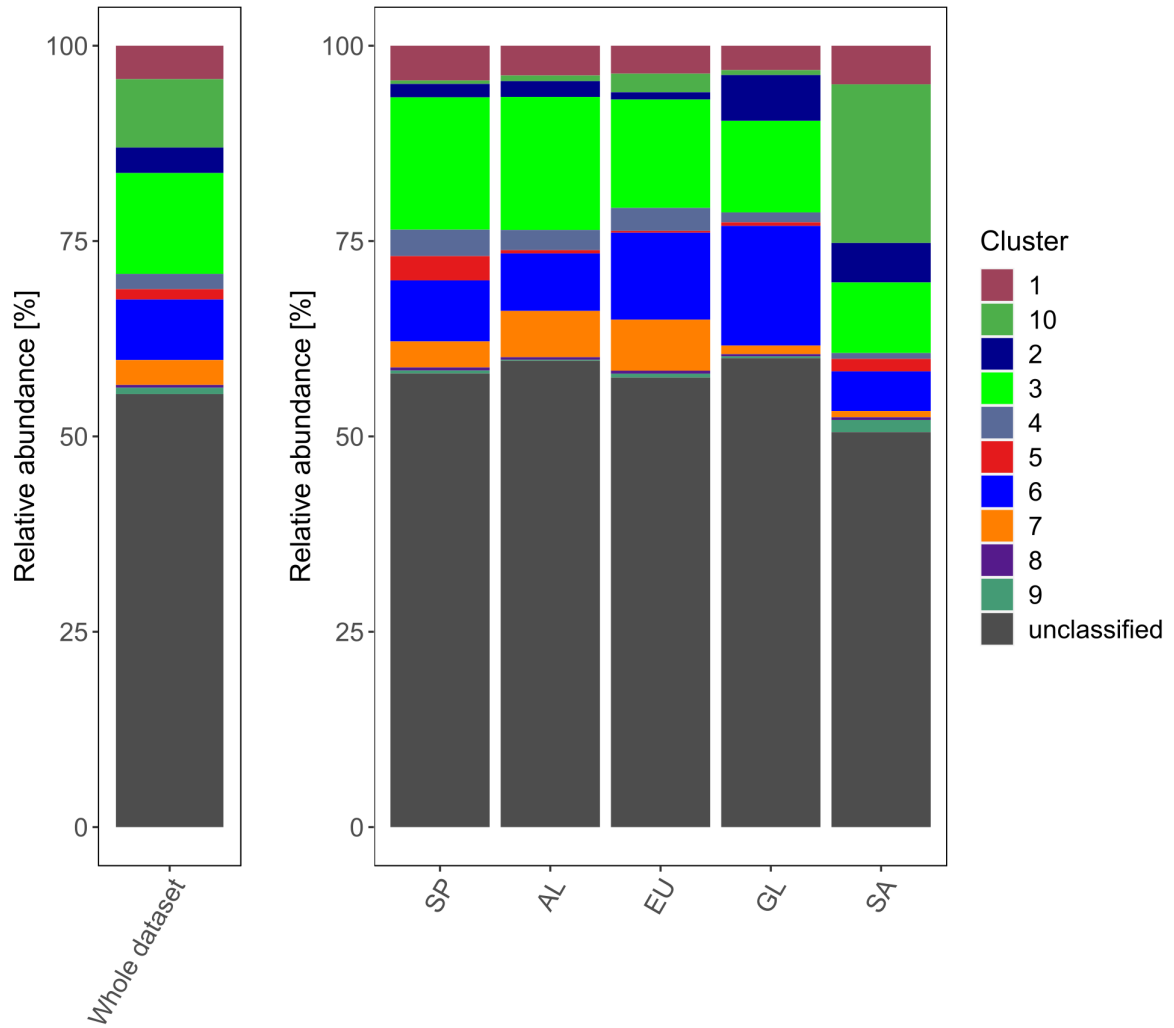
**Figure S4** Relationships between environmental predictors (x-axis) used for the models in Fig. 2 and trait CWMs (y-axis).



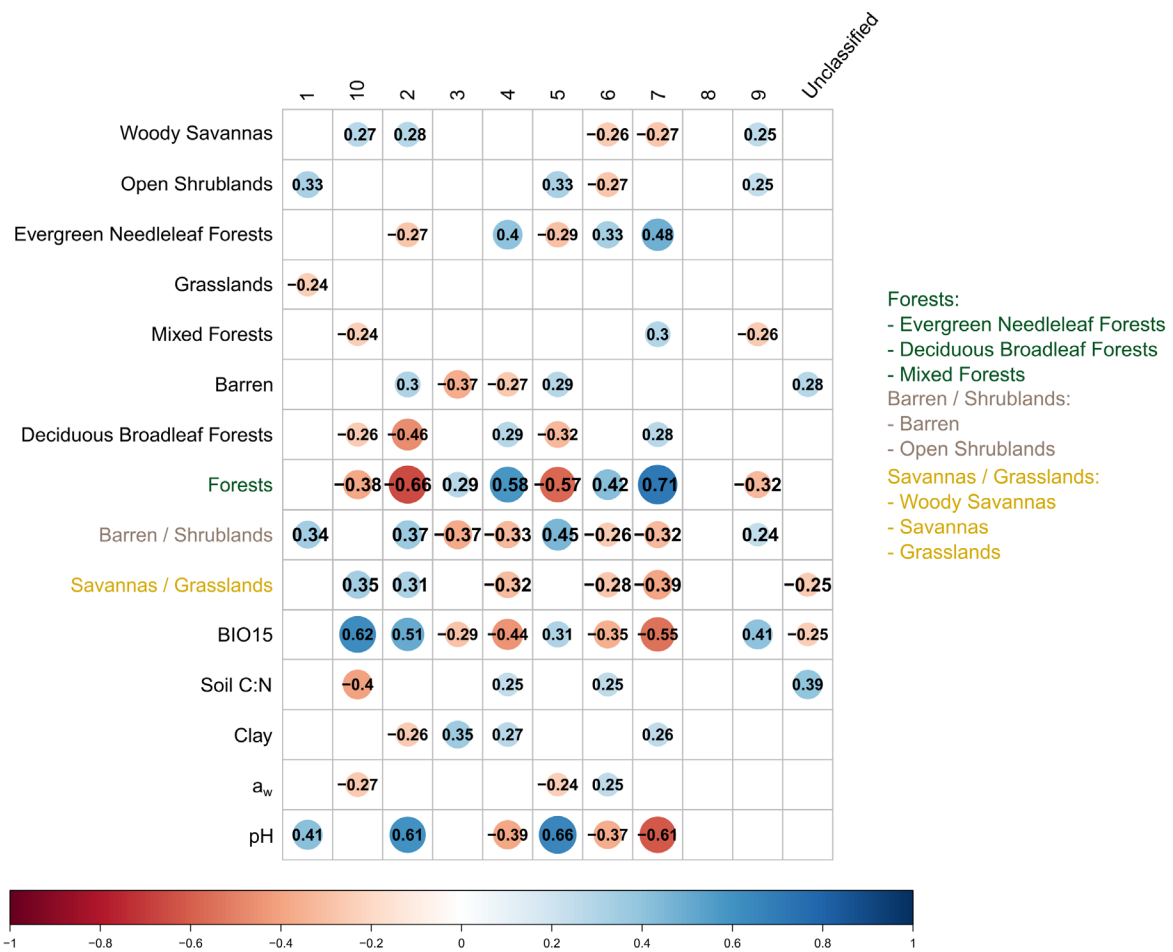
**Figure S5** Response plots for CWMs as a function of land cover class based on RFs and stepwise GLM. Only traits and models where land cover was among the five most important predictors are shown (see also Fig. 2).



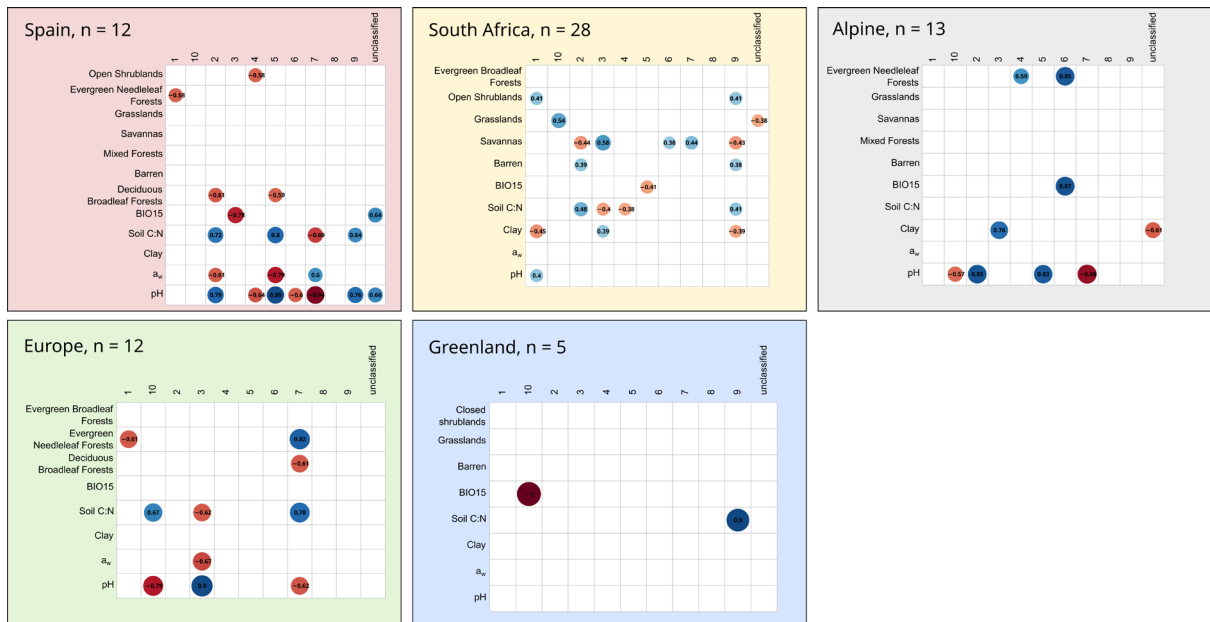
**Figure S6** Precipitation seasonality across land cover classes. The central mark indicates the median, upper and lower limits of boxes indicate the 25th and the 75th percentile. Grey points represent individual sites.



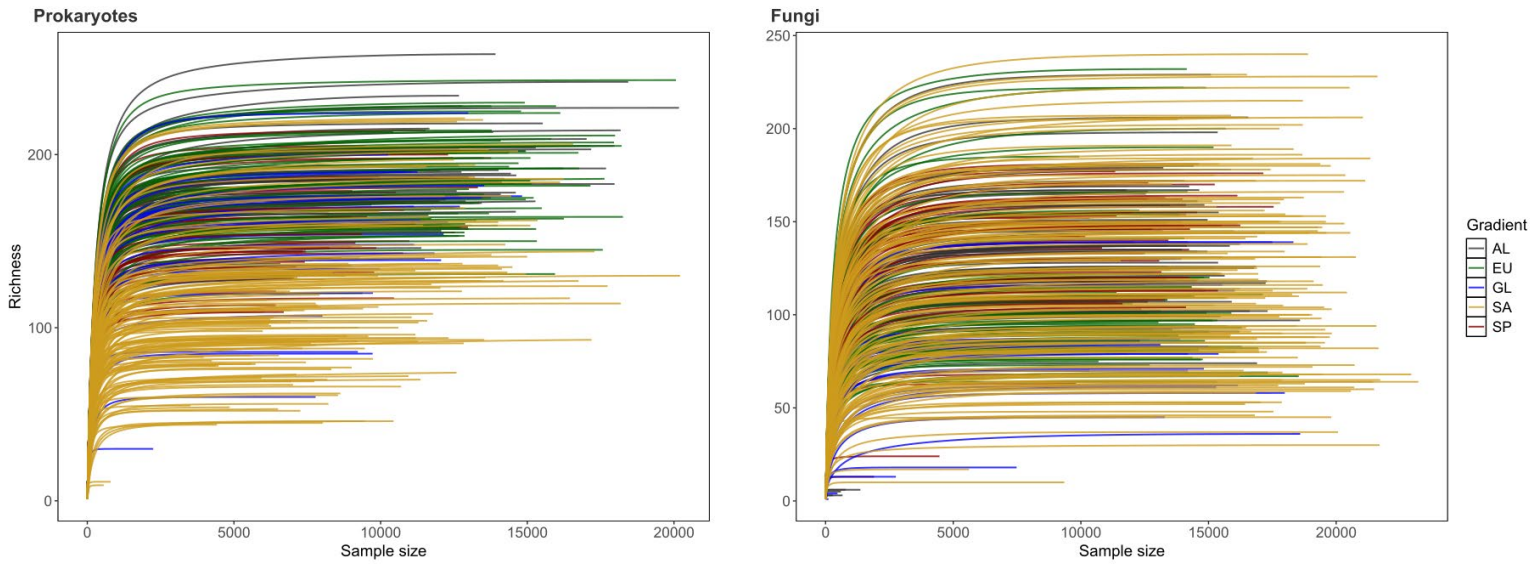
**Figure S7** Relative abundances of trait-based clusters across the whole dataset and individual gradients.



**Figure S8** Spearman correlations between abundances of trait clusters and environmental variables (n = 70). Significant correlations ( $P < 0.05$ ) with  $\rho \geq 0.2$  are shown. Only variables with at least one significant correlation are shown. The landcover categories Forests, Barren / shrublands and Savannas / Grasslands represent combined variables for the land cover classes indicated in the figure legend.  $a_w$  = water activity, BIO15 = precipitation seasonality.



**Figure S9** Spearman correlations between abundances of trait clusters and environmental variables for each gradient. Significant correlations ( $P < 0.05$ ) with  $\rho \geq 0.2$  are shown. Only variables with at least one significant correlation are shown.  $a_w$  = water activity, BIO15 = precipitation seasonality.



**Figure S10** Rarefaction curves for prokaryotic and fungal ASVs. Individual replicates are shown for each site ( $n = 5$ ,  $N = 349$ ). AL = alpine, EU = Europe, GL = Greenland, SA = South Africa, SP = Spain.

## Tables

**Table S1** Stepwise selection for constrained ordinations models of prokaryotic and fungal community structures based on Bray-Curtis similarities. Non-colinear environmental variables were included. Sequential addition of terms is shown. P-values were determined by a permutational test with 9999 permutations. BIO15 = precipitation seasonality, MAP = mean annual precipitation, T<sub>soil</sub> = in situ soil temperature at the time of sampling

<b>Prokaryotes</b>					
	R <sup>2</sup> <sub>adj</sub>	Df	AIC	F	P
Landcover	0.107805	9	239.2352	1.926374	0.0001
BIO15	0.145778	1	237.0141	3.667217	0.0001
pH	0.17044	1	235.7668	2.754015	0.0001
Soil C:N	0.188452	1	235.0128	2.287231	0.0001
MAP	0.199351	1	234.8273	1.775983	0.001
T <sub>soil</sub>	0.211017	1	234.5386	1.827994	0.0009
Silt	0.216608	1	234.7564	1.392496	0.0273
All variables	0.23432	NA	NA	NA	NA
<b>Fungi</b>					
	R <sup>2</sup> <sub>adj</sub>	Df	AIC	F	P
Landcover	0.072867	9	248.2417	1.60255	0.0001
BIO15	0.089825	1	247.7729	2.117954	0.0001
T <sub>soil</sub>	0.096552	1	248.057	1.439297	0.0015
pH	0.101811	1	248.431	1.339583	0.0064
Soil C:N	0.105571	1	248.8984	1.239608	0.0471
Litter	0.109521	1	249.3272	1.248418	0.0324
All variables	0.115935	NA	NA	NA	NA

**Table S2** Marginal tests for constrained ordinations models of prokaryotic and fungal community structures based on Bray-Curtis similarities. Non-colinear environmental variables were included. Marginal tests removing each term from the full model are shown. P-values were determined by a permutational test with 9999 permutations. BIO15 = precipitation seasonality, MAP = mean annual precipitation, T<sub>soil</sub> = in situ soil temperature at the time of sampling.

<b>Prokaryotes</b>				
	Sum of Squares	Df	F	P
Landcover	4.15	9	1.356767	0.0003
BIO15	0.70	1	2.060189	0.0029
pH	0.96	1	2.812266	0.0001
Soil C:N	0.60	1	1.7521	0.0039
MAP	0.63	1	1.863606	0.0084
T <sub>soil</sub>	0.63	1	1.844739	0.0048
Silt	0.47	1	1.392496	0.0638
Residual	18.37	54	NA	NA
<b>Fungi</b>				
	Sum of Squares	Df	F	P
Landcover	4.93	9	1.294536	0.0001
BIO15	0.59	1	1.400675	0.0106
T <sub>soil</sub>	0.55	1	1.290482	0.0238
pH	0.57	1	1.349631	0.0148
Soil C:N	0.53	1	1.256798	0.0199
Litter	0.53	1	1.248418	0.0434
All variables	23.28	55	NA	NA